OM protein - protein search, using sw model

Run on: January 24, 2003, 17:26:51

GenCore version 5.1.3
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Title: US-09-894-657-5
Perfect score: 2416
Sequence: 1 MDVENEQILNVNPADPDNLS..........RGRKRFVSEGDGGRLKPESY 469

Search time 35 seconds
(without alignments)
2761.031 Million cell updates/sec

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Database : SPTREMBL_21:*
   1: sp_archea:*
   2: sp_bacteria:*
   3: sp_fungi:*
   4: sp_human:*
   5: sp_invertebrate:*
   6: sp_mammal:*
   7: sp_mhc:*
   8: sp_organelle:*
   9: sp_phage:*
  10: sp_plant:*
  11: sp_rodent:*
  12: sp_virus:*
  13: sp_vertebrate:*
  14: sp_unclassified:*
  15: sp_rvirus:*
  16: sp_bacteriap:*
  17: sp_archeap:*

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2410	99.8	469	4	Q8TAR5	Q8tar5 homo sapien
2	2391	99.0	469	4	O15501	O15501 homo sapien
3	2351	97.7	469	11	Q61823	Q61823 mus musculu
4	2356	97.5	469	11	P97296	P97296 mus musculu
5	2332	96.5	458	4	Q99834	Q99834 homo sapien
6	2314	95.8	469	11	Q9JID1	Q9jid1 rattus norv
7	2078	86.0	467	13	Q98TX3	Q98tx3 gallus gall
8	859	35.6	463	5	O96944	O96944 suberites d
9	773	32.0	507	5	Q9VY91	Q9vy91 drosophila
10	438.5	18.1	729	10	Q94BR1	Q94br1 arabidopsis
11	419	17.3	729	10	Q9FMK4	Q9fmk4 arabidopsis
12	386	16.0	693	10	080548	080548 arabidopsis
13	369	15.3	702	10	08W4Q4	08w4q4 arabidopsis
14	369	15.3	942	10	Q9SZX0	Q9szx0 arabidopsis
15	364	15.1	618	10	O64378	O64378 arabidopsis
16	358.5	14.8	633	10	Q9STL9	Q9stl9 arabidopsis
17	137	5.7	787	10	Q41583	Q41583 tritium ae
18	135.5	5.6	1401	10	Q51KQ7	Q51kq7 arabidopsis
19	130	5.4	747	10	082233	082233 arabidopsis
20	130	5.4	747	10	Q8W4L4	Q8w4l4 arabidopsis
21	129	5.3	355	10	O23523	O23523 arabidopsis
22	129	5.3	1606	10	Q9LY39	Q9ly39 arabidopsis
23	126.5	5.2	645	4	Q96165	Q96165 homo sapien
24	126.5	5.2	1560	4	O43177	O43177 homo sapien
25	123	5.1	657	10	Q9SS38	Q9ss38 arabidopsis
26	122.5	5.1	907	4	P78344	P78344 homo sapien
27	122	5.0	726	10	Q9LTY1	Q9lty1 arabidopsis
28	121	5.0	907	2	P79398	P79398 oryctolagus
29	121	5.0	1004	2	Q93GI7	Q93gi7 ricketsia
30	119	4.9	1287	4	Q92549	Q92549 homo sapien
31	119	4.9	1824	5	Q9NBH3	Q9nbh3 strongyloce
32	117.5	4.9	823	10	Q9SUH8	Q9suh8 arabidopsis
33	117	4.8	136	6	Q95L46	Q95l46 bos taurus
34	117	4.8	351	17	Q980F5	Q980f5 sulfolobus
35	116.5	4.8	652	3	O75011	O75011 schizosacch
36	116	4.8	478	2	Q9AJL4	Q9ajl4 marine cfb-
37	115.5	4.8	751	10	Q9FJM7	Q9fjm7 arabidopsis
38	115.5	4.8	780	10	Q93ZT6	Q93zt6 arabidopsis
39	116	4.8	567	5	Q9NBH2	Q9nbh2 strongyloce
40	115	4.8	699	4	O15597	O15597 homo sapien
41	114.5	4.7	1585	4	O4432	O4432 homo sapien
42	113.5	4.7	1453	10	Q9C6F9	Q9c6f9 arabidopsis
43	112.5	4.7	1251	4	Q8TE62	Q8te62 homo sapien
44	112.5	4.7	1563	4	Q8TE61	Q8te61 homo sapien
45	111.5	4.6	479	11	Q8R2V4	Q8r2v4 mus musculu

ALIGNMENTS

RESULT 1
Q8TAR5

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ID   Q8TAR5      PRELIMINARY;      PRT;   469 AA.
AC   Q8TAR5;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Similar to programmed cell death 4 (neoplastic transformation
DE   inhibitor).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RA   Strausberg R.;
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC026104; AAH26104.1; -.
SQ   SEQUENCE   469 AA;   51797 MW;   8C72628AFFB1330B CRC64;
```

Query Match   99.8%;   Score 2410;   DB 4;   Length 469;
Best Local Similarity   99.8%;
Matches   468;   Conservative   0;   Mismatches   1;   Indels   0;   Gaps   0;

```
Qy    1  MDVENEQILNVNPADPDNLSDSLFSGDEENAGTEEVKNEINGNWISASSINEARINAKAK   60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1  MDVENEQILNVNPADPDNLSDSLFSGDEENAGTEEVKNEINGNWISAYSINEARINAKAK   60

Qy   61  RRLRKNSSRDSGRGDSVSDSGSDALRSGLTVPTSPKGRLLDRRSRSKGRGLPKKGGAGG   120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  RRLRKNSSRDSGRGDSVSDSGSDALRSGLTVPTSPKGRLLDRRSRSKGRGLPKKGGAGG   120

Qy  121  KGVWGTPGQVYDVEEVDVKDPNYDDDQOENCYETVVLPLDERAFEKTLTPIIQEYFEHGD   180
         ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db  121  KGVWGTPGQVYDVEEVDVKRDPNYDDDQOENCYETVVLPLDERAFEKTLTPIIQEYFEHGD   180

Qy  181  TNEVAEMLRDLNLGEMKSGVPVLAVSLALEGKASHREMTSKLLSDLCGTVMSTTDVEKSF   240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   181 TNEVAEMLRDLNLGEMKSGYPVLAVSLALEGKASHREMTSKLLSDLCGTVMSTTDVEKSF 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 TNEVAEMLRDLNLGEMKSGYPVLAVSLALEGKASHREMTSKLLSDLCGTVMSTTDVEKSF 240

Qy   241 DKLLKDLPELALDTPRAPQLVGQFIARAVGDGILCNTYIDSYKGTVDCVQARAALDKATV 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 DKLLKDLPELALDTPRAPQLVGQFIARAVGDGILCNTYIDSYKGTVDCVQARAALDKATV 300

Qy   301 LLSMSKGGKRKDSVWGSGGGGQQSVNHLVKEIDMLLKEYLLSGDISEAEHCLKELEVPHFH 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 LLSMSKGGKRKDSVWGSGGGGQQSVNHLVKEIDMLLKEYLLSGDISEAEHCLKELEVPHFH 360

Qy   361 HELVYEAIIMVLESTGESTFKMILDLLKSLWKSSTITVDQMKRGYERIYNEIPDINLDVP 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 HELVYEAIIMVLESTGESTFKMILDLLKSLWKSSTITVDQMKRGYERIYNEIPDINLDVP 420

Qy   421 HSYSVLERFVEECFQAGIISKQLRDLCPSRGRKRFVSEGDGGRLKPESY 469
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 HSYSVLERFVEECFQAGIISKQLRDLCPSRGRKRFVSEGDGGRLKPESY 469

RESULT 2
ID   O15501;   PRELIMINARY;   PRT;   469 AA.
AC   O15501;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Nuclear antigen H731-like protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BLOOD;
RX   MEDLINE=98430669; PubMed=9759869;
RA   Azzoni L., Zatsepina O., Abebe B., Bennett I.M., Kanakaraj P.,
RA   Perussia B.;
RT   "Differential transcriptional regulation of CD161 and a novel gene,
RT   197/15a, by IL-2, IL-15, and IL-12 in NK and T cells.";
RL   J. Immunol. 161:3493-3500(1998).
DR   EMBL; U96628; AAB67706.1; -.
DR   Pfam; PF02847; MA3; 2.
DR   SMART; SM00544; MA3; 2.
DR   InterPro; IPR003891; IF_eIF4G_MA3.
SQ   SEQUENCE 469 AA; 51713 MW; 8A75D7FA36C74496A CRC64;

Query Match   99.0%; Score 2391; DB 4; Length 469;
Best Local Similarity   99.1%;
Matches 465; Conservative   0; Mismatches   4; Indels   0; Gaps   0;

Qy   1 MDVENEQILNVNPADPDNLSDSLFSGDEENAGTEEVKNEINGNWISASSINEARINAKAK 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MDVENEQILNVNPADPDNLSDSLFSGDEENAGTEEVKNEINGNWISASSINEARINAKAK 60

Qy   61 RRLRKNSSRDSGRGDSVSDSGSDALRSGLTVPTSPKGRLLDRRSRSGKGRGLPKKGGAGG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 RRLRKNSSRDSGRGDSVSDSGSDALRSGLTVPTSPKGRLLDRRSRSGKGRGLPKKGGAGG 120

Qy   121 KGVWGTPGQVYDVEEVDVKDPNYDDDQENCVYETVVLPLDERAFEKTLTPIIQEYFEHGD 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 KGVWGTPGQVYDVEEVDVKDPNYDDDQENCVYETVVLPLDERAFEKTLTPIIQEYFEHGD 180

Qy   181 TNEVAEMLRDLNLGEMKSGYPVLAVSLALEGKASHREMTSKLLSDLCGTVMSTTDVEKSF 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 TNEVAEMLRDLNLGEMKSGYPVLAVSLALEGKASHREMTSKLLSDLCGTVMSTTDVEKSF 240

Qy   241 DKLLKDLPELALDTPRAPQLVGQFIARAVGDGILCNTYIDSYKGTVDCVQARAALDKATV 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 DKLLKDLPELALDTPRAPQLVGQFIARAVGDGILCNTYIDSYKGTVDCVQARAALDKATV 300

Qy   301 LLSMSKGGKRKDSVWGSGGGGQQSVNHLVKEIDMLLKEYLLSGDISEAEHCLKELEVPHFH 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 LLSMSKGGKRKDSVWGSGGGGQQSVNHLVKEIDMLLKEYLLSGDISEAEHCLKELEVPHFH 360

Qy   361 HELVYEAIIMVLESTGESTFKMILDLLKSLWKSSTITVDQMKRGYERIYNEIPDINLDVP 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 HELVYEAIIMVLESTGESTFKMILDLLKSLWKSSTITVDQMKRGYERIYNEIPDINLDVP 420

Qy   421 HSYSVLERFVEECFQAGIISKQLRDLCPSRGRKRFVSEGDGGRLKPESY 469
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 HSYSVLERFVEECFQAGIISKQLRDLCPSRGRKRFVSEGDGGRLKPESY 469

RESULT 3
ID   Q61823   PRELIMINARY;   PRT;   469 AA.
AC   Q61823;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   MA-3 protein.
DE   PDCD4 OR MA-3.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ICR; TISSUE=THYMUS;
RX   MEDLINE=96125207; PubMed=8543179;
RA   Shibahara K., Asano M., Ishida Y., Aoki T., Koike T., Honjo T.;
RT   "Isolation of a novel mouse gene MA-3 that is induced upon programmed
RT   cell death.";
RL   Gene 166:297-301(1995).
DR   EMBL; D50465; BAA09056.1; -.
DR   MGD; MGI:107490; Pdcd4.
DR   Pfam; PF02847; MA3; 2.
DR   SMART; SM00544; MA3; 2.
DR   InterPro; IPR003891; IF_eIF4G_MA3.
SQ   SEQUENCE 469 AA; 51702 MW; 6883BCE501I692P1 CRC64;

Query Match   97.7%; Score 2361; DB 11; Length 469;
Best Local Similarity   96.6%;
Matches 453; Conservative   9; Mismatches   7; Indels   0; Gaps   0;

Qy   1 MDVENEQILNVNPADPDNLSDSLFSGDEENAGTEEVKNEINGNWISASSINEARINAKAK 60
          |: :||||||||| ||||||||||||||||||||||||||:||||||||||||||||||||
Db   1 MDIENEQILNVNPPFDPDNLSDSLFSGDEENAGTEIKNEINGNWISASSINEARINAKAK 60

Qy   61 RRLRKNSSRDSGRGDSVSDSGSDALRSGLTVPTSPKGRLLDRRSRSGKGRGLPKKGGAGG 120
          |||||||||||||||:||||:|:|||:|||||||||||||||||||||||||||||||||
Db   61 RRLRKNSSRDSGRGDSDNGSEAVRSGVAVPTSPKGRLLDRRSRSGKGRGLPKKGGAGG 120

Qy   121 KGVWGTPGQVYDVEEVDVKDPNYDDDQENCVYETVVLPLDERAFEKTLTPIIQEYFEHGD 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 KGVWGTPGQVYDVEEVDVKDPNYDDDQENCVYETVVLPLDETAFEKTLTPIIQEYFEHGD 180

Qy   181 TNEVAEMLRDLNLGEMKSGYPVLAVSLALEGKASHREMTSKLLSDLCGTVMSTTDVEKSF 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 TNEVAEMLRDLNLGEMKSGYPVLAVSLALEGKASHREMTSKLLSDLCGTVMSTNDVEKSF 240

Qy   241 DKLLKDLPELALDTPRAPQLVGQFIARAVGDGILCNTYIDSYKGTVDCVQARAALDKATV 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 DKLLKDLPELALDTPRAPQLVGQFIARAVGDGILCNTYIDSYKGTVDCVQARAALDKATV 300

Qy   301 LLSMSKGGKRKDSVWGSGGGGQQSVNHLVKEIDMLLKEYLLSGDISEAEHCLKELEVPHFH 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 LLSMSKGGKRKDSVWGSGGGGQQSVNHLVKEIDMLLKEYLLSGDISEAFKMILDLLKSLWKSSTITVDQMKRGYERIYNEIPDINLDVP 360

Qy   361 HELVYEAIIMVLESTGESAFKMILDLLKSLWKSSTITVDQMKRGYERIYNEIPDINLDVP 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 HELVYEAIIMVLESTGESTFKMILDLLKSLWKSSTITVDQMKRGYERIYNEIPDINLDVP 420

Qy   421 HSYSVLERFVEECFQAGIISKQLRDLCPSRGRKRFVSEGDGGRLKPESY 469
          ||||||||||||||||| ||||||||||||||||||||||||||||||
Db   421 HSYSVLERFVEECFQAGIIWKQLRDLCPSRGRKRFVSEGDGGRLKPESY 469

RESULT 4
ID   P97296
AC   P97296;
DT   01-MAY-1997 (TrEMBLrel. 03, Created)
DT   01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Topoisomerase-inhibitor suppressed, complete CDS.
GN   PDCD4 OR TIS.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98382539; PubMed=9714845;
RA   Onishi Y., Hashimoto S., Kizaki H.;
RT   "Cloning of the TIS gene suppressed by topoisomerase inhibitors.";
RL   Gene 215:453-459(1998).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97069646; PubMed=8912629;
RA   Onishi Y., Kizaki H.;
RT   "Molecular cloning of the genes suppressed in RVC lymphoma cells by
RT   topoisomerase inhibitors.";
RL   Biochem. Biophys. Res. Commun. 228:7-13(1996).
DR   EMBL; D86344; BAA13072.1; -.
DR   EMBL; AB010139; BAA32356.1; -.
DR   EMBL; AB010129; BAA32356.1; JOINED.
DR   EMBL; AB010130; BAA32356.1; JOINED.
DR   EMBL; AB010131; BAA32356.1; JOINED.
DR   EMBL; AB010132; BAA32356.1; JOINED.
DR   EMBL; AB010133; BAA32356.1; JOINED.
DR   EMBL; AB010134; BAA32356.1; JOINED.
DR   EMBL; AB010135; BAA32356.1; JOINED.
DR   EMBL; AB010136; BAA32356.1; JOINED.
DR   EMBL; AB010137; BAA32356.1; JOINED.
DR   EMBL; AB010138; BAA32356.1; JOINED.
DR   MGD; MGI:107490; Pdcd4.
DR   InterPro; IPR003891; IF_eIF4G_MA3.
DR   Pfam; PF02847; MA3; 2.
DR   SMART; SM00544; MA3; 2.
KW   Isomerase; Topoisomerase.
SQ   SEQUENCE 469 AA; 51742 MW; FBC5561BA4615D2D CRC64;

Query Match   97.5%; Score 2356; DB 11; Length 469;
Best Local Similarity   96.6%;
Matches 453; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

Qy   1 MDVENEQILNVNPADPDNLSDSLFSGDEENAGTEEVKNEINGNWISASSINEARINAKAK 60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MDIENEQTLNVNPTDPDNLSDSLFSGDEENAGTEEIKNEINGNWISASTINEARINAKAK 60

Qy   61 RRLRKNSSRDSGRGDSVSDSGSDALRSGGLTVPTSPKGRLLDRRSRSGKGRGLPKKGGAGG 120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 RRLRKNSSRDSGRGDSVSDNGSEAVRSGVAVPTSPKGRLLDRRSRSGGRGRGLPFKKGGAGG 120

Qy   121 KGVWGTPGQVYDVDVEEVDVKDPNYDDDQENCYVETVVLPLDERAFEKTLTPIIQEYFEHGD 180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 KGVWGTPGQVVDVEEVDVKDPNYDDDQENCYETVVLPLDETAFEKTLTPIIQEYFEHGD 180

Qy   181 TNEVAEMLRDLNIGEMKSGVPVLAVSLALEGKASHREMTSKLLSDLCGTVMSTTDVEKSF 240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 TNEVAEMLRDLNIGEMKSGVPVLAVSLALEGKASHREMTSKLLSDLCGTVMITNDVEKSF 240

Qy   241 DKLLKDLPELALDTPRAPQLVGQFIARAVGDGILCNTYIDSYKGTVDCVQARAALDKATV 300
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 DKLLKDLPELALDTPRAPQLVGQFIARAVGDGILCNTYIDSYKGTVDCVQARAALDKATV 300

Qy   301 LLSMSKGGKRRDSVWGSGGGQQSVNHLVKEIDMLLKEYLLSGDISEAEHCLKELEVPHFH 360
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 LLSMSKGGKRRDSVWGSGGGQQSVNHLVKEIDMLLKEYLLSGDISEAEHCLKELEVPHFH 360

Qy   361 HELIVYEAIIMVLESTGESTFKMILDLLKSLWKSSTITVDQMKRGYERIYNEIPDINLDVP 420
           |||:||||||||||||||||:|||||||||||||||||:||||||||||||||||||||||
Db   361 HELVYEAIIMVLESTGESAFKMILDLLKSLWKSSTITIDQMKRGYERIYNEIPDINLDVP 420

Qy   421 HSYSVLERFVEECFQAGIISKQLRDLCPSRGRKRFVSEGDGGRLKPESY 469
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 HSYSVLERFVEECFQAGIISKQLRDLCPSRGRKRFVSEGDGGRLKPESY 469

RESULT 5
ID   Q99834
AC   Q99834;
DT   01-MAY-1997 (TrEMBLrel. 03, Created)
DT   01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Nuclear antigen H731.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Matsuhashi S., Yoshinaga H., Yatsuki H., Tsugita A., Hori K.;
RT   "Isolation of a novel gene from a human cell line with Pr-28 MAb which
RT   recognizes a nuclear antigen involved in the cell cycle.";
RL   Res. Commun. Biochem. Cell Biol. 1:109-120(1997).
DR   EMBL; U83908; AAB42218.1; -.
DR   InterPro; IPR003891; IF_eIF4G_MA3.
DR   Pfam; PF02847; MA3; 2.
DR   SMART; SM00544; MA3; 2.
SQ   SEQUENCE 458 AA; 50590 MW; 8D3D850B9D68C1D5 CRC64;

Query Match   96.5%; Score 2332; DB 4; Length 458;
Best Local Similarity   99.6%;
Matches 452; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy   16 PDNLSDSLFSGDEENAGTEEVKNEINGNWISASSINEARINAKAKRRLRKNSSRDSGRGD 75
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5 PDNLSDSLFSGDEENAGTEEVKNEINGNWISASSINEARINAKAKRRLRKNSSRDSGRGD 64

Qy   76 SVSDSGSDALRSGGLTVPTSPKGRLLDRRSRSGKGRGLPKKGGAGGKGVWGTPGQVYDVEE 135
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   65 SVSESGSDALRSGGLTVPTSPKGRLLDRRSRSGGAGGKGVWGTPGQVVDVEE 124

Qy   136 VDVKDPNYDDDQENCYVETVVLPLDERAFEKTLTPIIQEYFEHGDTNEVAEMLRDLNIGE 195
           ||||||||||||||:|||||||||||||||||||||||||||||||||||||||||||
Db   125 VDVKDPNYDDDQENCYETVVLPLDERAFEKTLTPIIQEYFEHGDTNEVAEMLRDLNIGE 184

Qy   196 MKSGVPVLAVSLALEGKASHREMTSKLLSDLCGTVMSTTDVEKSFDKLLKDLPELALDTP 255
           |||||||||||||||||||||||||||||:|||:|||||||||||||||||||||||||
Db   185 MKSGVPVLAVSLALEGKASHREMTKLLSDLCGTVMSTTDVEKSFDKLLKDLPELALDTP 244

Qy   256 RAPQLVGQFIARAVGDGILCNTYIDSYKGTVDCVQARAALDKATVLLSMSKGGKRRDSVW 315
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   245 RAPQLVGQFIARAVGDGILCNTYIDSYKGTVDCVQARAALDKATVLLSMSKGGKRRDSVW 304

Qy   316 GSGGGQQSVNHLVKEIDMLLKEYLLSGDISEAEHCLKELEVPHFHHELVYEAIIMVLEST 375
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   305 GSGGGQQSVNHLVKEIDMLLKEYLLSGDISEAEHCLKELEVPHFHHELVYEAIIMVLEST 364

Qy   376 GESTFKMILDLLKSLWKSSTTVDQMKRGYERIYNEIPDINLDVPHSYSVLERFVEECFQ 435
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   365 GESTFKMILDLLKSLWKSSTTVDQMKRGYERIYNEIPDINLDVPHSYSVLERFVEECFQ 424

Qy   436 AGIISKQLRDLCPSRGRKRFVSEGDGGRLKPESY 469
           |||||||||||||||||||||||||||||||||
Db   425 AGIISKQLRDLCPSRGRKRFVSEGDGGRLKPESY 458

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RESULT 6
ID   Q9JID1      PRELIMINARY;   PRT;   469 AA.
AC   Q9JID1;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Death-upregulated gene.
DUG.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Goke A., Goke R., Wilmen A., Goke B., Chen Y.;
RT   "DUG, a novel homolog of translation initiation factor 4G, regulates
RT   cell growth and apoptosis.";
RL   Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF239739; AAF73961.1; -.
DR   InterPro; IPR003891; IF_eIF4G_MA3.
DR   Pfam; PF02847; MA3; 2.
DR   SMART; SM00544; MA3; 2.
SQ   SEQUENCE   469 AA;  51796 MW;  2B0B007CDEB9FD89 CRC64;

  Query Match             95.8%;  Score 2314;  DB 11;  Length 469;
  Best Local Similarity   94.7%;
  Matches  444;  Conservative   15;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 MDVENEQILNVNPADPDNLSDSLFSGDEENAGTEEVKNEINGNWISASSINEARINAKAK 60
              ::|:|||||||||| ||||||||||||||||||||||:|||:|:|||||||:|||||||||
Db          1 MDIENEQILNVNPPTDPDNLSDSLFSGDEENAGTEEIKNEIGNGNWISASTINEARINAKAK 60

Qy         61 RRLRKNSSRDSGRGDSVSDSGSDALRSGLTVPTSPKGRLLDRRSRSGKGRGLPKKGGAGG 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 RRLRKNSSRDSGRGDSVSDSGSDALRSGLTVPTSPKGRLLDRRSRSGKGRGLPKKGGAGG 120

Qy        121 KGVWGTPGQVYDVEEVDVKDPNYDDDQENCVYETVVLPLDERAFEKTLTPIIQEYFEHGD 180
              |||||||||||||||:||||||||||||||||||||||||||:|||||||||||||||||
Db        121 KGVWGTPGQVYDVEKVDVKDPNYDDDQENCVYETVVLPLDETAFEKTLTPIIQEYFEHGD 180

Qy        181 TNEVAEMLRDLNLGEMKSGVPVLAVSLALEGKASHREMTSKLLSDLCGTVMSTTDVEKSF 240
              |||||||||||||:|||||||||||||||||||||||||||||||||||||||:||||||
Db        181 TNEVAEMLRDLNIWEMKSGVPVLAVSLALEGKASHREMTSKLLSDLCGTVMSTNDVEKSF 240

Qy        241 DKLLKDLPELALDTPRAPQLVGQFIARAVGDGILCNTYIDSYKGTVDCVQARAALDKATV 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 DKLLKDLPELALDTPRAPQLVGQFIARAVGDGILCNTYIDSYKGTVDCVQARAALDKATV 300

Qy        301 LLSMSKGGKRKDSVWGSGGGQQOSVNHLVKEIDMLLKEYLLSGDISEAEHCLKELEVPHFH 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LLSMSKGGKRKDSVWGSGGGQQOSVNHLVKEIDMLLKEYLLSGDISEAEHCLKELEVPHFH 360

Qy        361 HELVYEAIIMVLESTGESTFKMILDLLKSLWKSSTTIVDQMKRGYERIYNEIPDINLDVP 420
              ||||:|||:|||||||||:|||:|:|||||||||||:|||||||||||||||||||||||
Db        361 HELVEAIVMVLESTGESAFKMMLGLLKSLWKSSTIIDQMKRGYERIYNEIPDINLDVP. 420

Qy        421 HSYSVLERFVEECFQAGIISKQLRDLCPSRGRKRFVSEGDGGRLKPESY 469
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 HSYSVLERFVEECFQAGIISKQLRDLCPSRGRKRFVSEGDGGRLKPESY 469
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RESULT 7
ID   Q98TX3      PRELIMINARY;   PRT;   467 AA.
AC   Q98TX3;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Programmed cell death 4 protein.
PDCD4.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21214412; PubMed=11313950;
RA   Schlichter U., Burk O., Worpenberg S., Klempnauer K.-H.;
RT   "The chicken Pdcd4 gene is regulated by v-Myb.";
RL   Oncogene 20:231-239(2001).
DR   EMBL; AF321288; AAK09354.1; -.
DR   InterPro; IPR003891; IF_eIF4G_MA3.
DR   Pfam; PF02847; MA3; 2.
DR   SMART; SM00544; MA3; 2.
SQ   SEQUENCE   467 AA;  51707 MW;  361B04FFA47B99E8 CRC64;

  Query Match             86.0%;  Score 2078;  DB 13;  Length 467;
  Best Local Similarity   84.9%;  Pred. No. 6.2e-139;
  Matches  398;  Conservative   39;  Mismatches   30;  Indels    2;  Gaps    2;

Qy          1 MDVENEQILNVNPADPDNLSDSLFSGDEENAGTEEVKNEINGNWISASSINEARINAKAK 60
              |:|:|:||:||| |||:|::||:||||||||:|:|:||:||:|:||||||:|:|:|||||
Db          1 MEIEKQHYV-ISTVEVENLSDALFSGDEENGGSEERKTEINGNNWIPATSTEAKINAKAK 59

Qy         61 RRLRKNSSRDSGRGDSVSDSGSDALRSGLTVPTSPKGRLLDRRSRSGKGRGLPKKGGAGG 120
              ||||||||||||||||||:   :|:|||:|:||||||::|||||||||||||||||||||
Db         60 RRLRKNSSRDSGRGDSVSENG-ETQKAGILVVPISPKGVLDRRSRSGKGRGLPKKGGAGG 118

Qy        121 KGVWGTPGQVYDVEEVDVKDPNYDDDQENCVYETVVLPLDERAFEKTLTPIIQEYFEHGD 180
              |||||||||||||||||:|:||||||||||||||||||||||||||||||||||||||||
Db        119 KGVWGTPGQVYDVEEVDIKRDPNYDDDQENCVYETVVLPLDERAFEKTLTPIIQEYFEHGD 178

Qy        181 TNEVAEMLRDLNLGEMKSGVPVLAVSLALEGKASHREMTSKLLSDLCGTVMSTTDVEKSF 240
              ||||:|||:||||||| :|||||||||||||||||||||||||||||||::|:||||||
Db        179 TNEVSEMLKDLNLGEMKYSVPVLAVSLALEGKASHREMTSKLLSDLCGTVVSKTDVEKSF 238

Qy        241 DKLLKDLPELALDTPRAPQLVGQFIARAVGDGILCNTYIDSYKGTVDCVQARAALDKATV 300
              |||||||| |:||:|||||||||||||||||||:::|||:|||||||||||||||||:|||
Db        239 DKLLKDLPDLVLDSPRAPQLVGQFIARAVGDGILSSTYIDGYKGTVDCVQARAALDRATV 298

Qy        301 LLSMSKGGKRKDSVWGSGGGQQOSVNHLVKEIDMLLKEYLLSGDISEAEHCLKELEVPHFH 360
              |||::|||||:|:::|||||||||||:||||||||||||||||||:|||:|||:|||||||
Db        299 LLSVTKGGKRIDNYWGSGGGQQOSVKHLVKEIDMLLKEYLLSGDLLEAERCLQELEVPHFH 358

Qy        361 HELVYEAIIMVLESTGESTFKMILDLLKSLWKSSTTIVDQMKRGYERIYNEIPDINLDVP 420
              ||||:|||:|||||||| |||:|:|||||||:||:|||||||||||:|:||||||||||
Db        359 HELVEAIVMVLESTGEKIFKMMLDLLKSLSRSSVITMDQMKRGYERVCEIFPDINLDVP 418

Qy        421 HSYSVLERFVEECFQAGIISKQLRDLCPSRGRKRFVSEGDGGRLKPESY 469
              |||||||||||||||||||||:||||||||||||||||||||||||||
Db        419 HSYSVLERFVEECFQAGIISKPLRDLCPSRGRKRFVSEGDGGRLKPESY 467
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RESULT 8
ID   O96944      PRELIMINARY;   PRT;   463 AA.
AC   O96944;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   MA3 protein.
OS   Suberites domuncula (Sponge).
OC   Eukaryota; Metazoa; Porifera; Demospongiae; Tetractinomorpha;
OC   Hadromerida; Suberitidae; Suberites.
OX   NCBI_TaxID=55567;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Wagner C., Steffen R., Koziol C., Batel R., Lacorn M., Steinhart H.,
RA   Simat T., Mueller W.E.G.;
RT   "Apoptosis in marine sponges: A biomarker for environmental stress
RT   (cadmium and bacteria).";
RL   Mar. Biol. 131:411-421(1998).
DR   EMBL; Y15421; CAA75614.1; -.
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DR   InterPro; IPR003891; IF_eIF4G_MA3.
DR   Pfam; PF02847; MA3; 2.
DR   SMART; SM00544; MA3; 2.
SQ   SEQUENCE   463 AA;  50765 MW;  BE82D8CCAEC8DEF8 CRC64;

Query Match             35.6%;  Score 859;  DB 5;  Length 463;
Best Local Similarity   40.7%;  Pred. No. 1.2e-52;
Matches  200;  Conservative  83;  Mismatches 152;  Indels  56;  Gaps  12;

Qy       1 MDVENEQILNVNPADPDNLSDSLFSGDEENAGTEEVKNEINGNWI------------------SAS 48
           : |||       :|||: |   |||||  ||  ||                             ||
Db       4 MEVEPQQVNGF------------GGSKNSPT---NGHHVQFPDTTVKVVTMPATS 42

Qy      49 SINEARINAKAKRRLRKNSSRDSGSRGDSVSDSGSDSDALRSGLIVPTSP----KGRLLDRRS 104
           :: ||:|  | |    |||:| |||: |        |  ||| |  |  :     |||||||
Db      43 TOPSSRPKHRARRARVPANDLIGEDETSSVSST-------TKPPSPSKLKMADKERRS 95

Qy     105 RSGKGRGLPKKGGAGGKGVWGTPGQVVDVEEV---DVKDPNYDD-DQENCVYETVVLPLDE 161
           ||||:    | ||    :||| |    |  ::|   : ||  ||  |||:|  || | :
Db      96 RSGR-RQQPKKGGGGGKGTWGNITDEMYAEPVTHDTHDPNDSVDEDDATY--LVSPSSS 152

Qy     162 RA----FEKTLTPIIQEYFEHGDTNEVAEMLRDLNLGEMKSGVPVLAVSLALEGKASHRE 217
           :|       || |  |||| ||||||||:|||||||||  | :||| | :|||::||::
Db     153 QMSALDFEKTAIEIKYEYFDHGDTQEVASSLEELSIKNIKHEVVRIVVTLALEEKAANRE 212

Qy     218 MTSKLLSDLCGTVMSTTDVEKSFDKLLKDLPELALDTPRAPQLVGQFIARAVGDGILCNT 277
           |  |||||| ||| ||||:|||||||||||||||||| |  ||   |  |  || |  :
Db     213 KVSVLLSDLYGQVINGREVAKGFDIILSQLNDLILDTPDAASVIGNFIARCVADDCLPPA 272

Qy     278 YIDSYKGTVDCVQARAALDKATVLLSMSKGGKRKDSVWGSSGGQQSVNHLVKEIDMLLKE 337
           | :|      |||  |||| ||| |||||||||||||||||||| |||| || |  |||:
Db     273 FVSNHTDVTN-EQIIVALKRAQLLSIKHSIARLDNVWGVGGGQRPVWFLISKMNLLKE 331

Qy     338 YLLSGDISEAEHCLKELEVPHFHHELVYEAIIMVLESTGESTFKMILDLLKSLWKSSTIT 397
           |||||||    |||:| |||||||||||||| |||| |||| ||||||| |::||:||
Db     332 YLSSGDCEEATRCLRDLEVPHFHHELVHEALVLVMEDATHDHTAKMIASLLOHMGQTGVIS 391

Qy     398 VDQMKRGYERIYNEIPDINLDVPHSYSVLERFVEECFQAGIISKQLRDLCPSGRKRFVS 457
           |||||||| ||||||||| |||| |:||||  |  ||: |||: :|||:||||||||
Db     392 TDQFNSGIMRVFSDMTDIVLDIPNAVHTLISKFVERGAAAGFVSRQIAEEIPSRGRKRYVS 451

Qy     458 EGDGGRLK-PE 467
           |||||:||  ||
Db     452 EGDGGAIKSPE 462
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RESULT 9
Q9VY91

ID   Q9VY91        PRELIMINARY;  PRT;  507 AA.
AC   Q9VY91;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   CG10990 protein.
GN   CG10990.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BERKELEY;
RX   MEDLINE=20196006; PubMed=10731132;
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA   Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA   Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA   Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA   Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA   Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA   Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA   Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA   Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
DR   EMBL; AE003493; AAF48312.1;
DR   FlyBase; FBgn0030520; CG10990.
DR   InterPro; IPR003891; IF_eIF4G_MA3.
DR   Pfam; PF02847; MA3; 2.
DR   SMART; SM00544; MA3; 2.
DR   PROSITE; PS00626; RCC1_2; UNKNOWN_1.
SQ   SEQUENCE   507 AA;  58817 MW;  388E008542Z7DADD3 CRC64;

Query Match             32.0%;  Score 773;  DB 5;  Length 507;
Best Local Similarity   35.8%;  Pred. No. 1.7e-46;
Matches  189;  Conservative  93;  Mismatches 154;  Indels  92;  Gaps  17;

Qy       1 MDVE--NEQILN----VNPADPDNLSDSLFSGDEENAGTEEVKN-EINGNWISASS---- 49
           :||:  |||||     :|:|| |  ||||||||||||||||||   |||||||:|||
Db       1 MEVESSNNKRATNGGRHFTPPSDSDSKESSV-----ERELNEEIEAVELNGSGGGHSNGH 55

Qy      50 ------INEARINAKAKRRLRKNSSRDSGSRGDSVSDS---------GSDALRSGLI-VPT 93
                 || |  | | |     |||:| |||: |||||          ||  ||| |  |
Db      56 VKKLMAVEDGRIKRAKRLIQRQNSGSGGSANQTNGAGAGGAHGASVMPLGINRIMP 115

Qy      94 SPKGRLL-----DRRSRS-GKGRGLPKKGGAGGKGVWGTPG----QYYDVEVDVKD 140
           ||  |||     |:|| | ||||||||||||||||||| |||    |   :  :|:
Db     116 SPGGYVVPHRWKNSRSRRFINRGRGLPKKGGGGGKGVWGLPGSEALAEVVE----DEND 171

Qy     141 PNYDDD--QENCVYETVVLPLDERAFEKTLTPIIQEYFEHGDTNEVAEMLRDLNLGEMKS 198
           |||:    |||:|| ||||||||:  |||||||:||||||||||||||||||||||||||
Db     172 PNYDSECNDRNVELREVTIEITREEFFKLAEPIVLEYYEHGDPHEVALSFDEILGQAPMRE 231

Qy     199 GVPVLAVSLALEGKASHREMTSKLLSDLCGTVMSTTDVEKSFDKLLKDLPELALDTPRAP 258
           |||| | :|||| |  ||||:: ||||| |||:|||| |||||||||||||||| ||||
Db     232 HVTSILVEIAMDHKDSQREMTSVLISDLYGRVITGKDIEKGFNMLLANLPDLVLDTPEAP 291

Qy     259 QLVGQFIARAVGDGILCNTYIDSYKGTVDCV--------QARAALDKAT 299
           ||| |:|| || || |  || :||||||||          |||:||||
Db     292 IMLGNFMARAVAD----------DCIPPKFVAKSGEELRHLGLGEHAEQALRRAD 336

Qy     300 VLLSMSGGKRKDSVWGSGGGGQQSVNHLVKEIDMLLKEYLLSGDISEAEHCLKELEVPHF 359
           ||||| |||:|||||| |||||| |||| || |  |||:||||||:  | |||:| ||||
Db     337 SLI-YKHVWAHLDNVWGMGGPLRPVKTITMQMELLIKEYLSSRDVAEAQRCLRALEVPHY 395

Qy     360 HHELVYEAIIMVLESTGESTFKMILDLLKSLWKSSTITVDQMKRGYERIYNEIPDINLDV 419
           ||||||||| |:||||||||||||||||:||||||||||:|||||||||||||||| |||
Db     396 HHELVYEAIVMTLESLSQTTEEAMCELLKQLDLTCLVLPAGMEQQFLRAFDDMADIVLDV 455
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Qy  420 PHSYSVLERFVEECFQAGIISKQLRDLCPSRGRK-RFVSEGDGGGRLKP 466
            :|||       ||  || ||   | | |  ||| ||  |||  ||
Db  456 PLAYILDRFVERCNRAGFLTDKIINNVPSRTQAFRF-----GGRRP 498

RESULT 10
ID   Q94BR1         PRELIMINARY;       PRT;    702 AA.
AC   Q94BR1;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Putative topoisomerase.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
RA   Dale J.M., Gibson H.A., Goldsmith A.D., Jiang P.X., Lee J.M.,
RA   Quach H.L., Tang C., Toriumi M., Yu G., Bowser L., Carnicni F.,
RA   Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T., Kamiya A.,
RA   Karlin-Neumann G., Kawai J., Kim C., Koesema E., Lam B., Lin J.,
RA   Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
RA   Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Tracy S.E.,
RA   Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
RT   "Full length cDNA of gene MDC12.16/At5g63190 (GI:10177300).";
RL   Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
SQ   SEQUENCE   702 AA;  77556 MW;  4FB63FB12263C6D9 CRC64;

Query Match             18.18%;  Score 438.5;  DB 10;  Length 702;
Best Local Similarity   31.6%;  Pred. No. 1.4e-22;
Matches  130;  Conservative  67;  Mismatches  172;  Indels  43;  Gaps  13;

Qy   74 GDSVSDSGGSDALRSGLTV--PFSPKGRLLD------RSRSRGKGRGLPKKGRAGGKGVWG 125
Db   24 GSLSSSPKSHTLFADLNIKSPIGGKGPVAGIPNRHVRRTHSGKHIRV-KKEGAGGKGIW- 81

Qy  126 TPGQVDVEE---VDVKDPNYD--DDQENCVYETVVLPLDERAFEKITPIIQEYFEH 178
Db   82 --GKLLDTDDGDSCIDKNDPNVDSGEDAYDGLVDSPVSDPLND--YKKSVVSIIDEYFST 137

Qy  179 GGTNEVAEMLRDLNLGEMKSGVPVLAVSLALEGKASHREMTSKLLSDLCGTVMSTTDVEK 238
Db  138 GDVKVAASDLRELGSSEYHPYFTKRLVSMAMDRHDKEKEMASVLLSALYADVILPDQIRD 197

Qy  239 SFDKLLKDLPELALDTPRAPQLVGQFIARAVGDGILCNFYI--------DSYKGTVDCVQ 290
Db  198 GFIRLRSVDDLAVDILDAVVNLALFIARAIVDEILPPVFLVRSKKILPESCKGFQVIVT 257

Qy  291 ARAALDKATVLLSMSKGGKRKDSVWGSCGGQQOSVNHLVKEIDMLLKEYLLSGDISEAEHC 350
Db  258 AEKS--------YLSAPHHAELVEKKWG--GSTHTTVEETKKKISEILKEYVENGDTYEACRC 310

Qy  351 LKELEVPHFHELVEYEAIIMVLES-TGESTFKMILDLLKSLWKSSTIIVDQMKRGYERIY 409
Db  311 IRELGVSFFHHEVVKRALVLAMDSPTAES---LVLKLKETAEEGLISSSQMVKGFFRVA 367

Qy  410 NEIPDINLDVPHSYSVLERFVEECFQAGIISKQLRDLCPSRGRKRFVSEGDG 461
Db  368 ESLDDLALDIPSAKKLFPDSIVPKAISGGWLDDSFKITSDQDGEK---SSQDG 416
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AC   Q9FMK4;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Topoisomerase-like protein.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=COLUMBIA;
RX   MEDLINE=98162728; PubMed=9501997;
RA   Nakamura Y., Sato S., Kaneko T., Kotani H., Asamizu E., Miyajima N.,
RA   Tabata S.;
RT   "Structural analysis of Arabidopsis thaliana chromosome 5. III.
RT   Sequence features of the regions of 1,191,918 bp covered by seventeen
RT   physically assigned P1 clones.";
RL   DNA Res. 4:401-414(1997).
DR   EMBL; AB008265; BAB10561.1; -.
DR   InterPro; IPR003891; IF_eIF4G_MA3.
DR   Pfam; PF02847; MA3; 4.
DR   SMART; SM00544; MA3; 4.
KW   Isomerase.
SQ   SEQUENCE   729 AA;  80705 MW;  B83717D4372BFC90 CRC64;

Query Match             17.3%;  Score 419;  DB 10;  Length 729;
Best Local Similarity   29.5%;  Pred. No. 3.4e-21;
Matches  129;  Conservative  67;  Mismatches  174;  Indels  68;  Gaps  13;

Qy   74 GDSVSDSGGSDALRSGLTV--PFSPKGRLLD------RSRSRGKGRGLPKK------ 114
Db   24 GSLSSSPKSHTLFADLNIKSPIGGKGPVAGIPNRHVRRTHSGKHIRVKKVKRLKFSVEEF 83

Qy  115 -----------KGGAGGKGVWGTPGQVTDVEE-----VDVKDPNYD--DDQENCVY 152
Db   84 KCVGDIWFTYVAMISAEGGAGGKGTW------GKLLDTDDGDSCIDKNDPNYDSGEDAYDGLVD 140

Qy  153 ETVVLPLDERAFEKTLPIIQEYFEHGDTNEVAEMLRDLNLGEMKSGVPVLAVSLALEGK 212
Db  141 SPVSDPLND--YKKSVVSIIDEYFSTGDVKVAASDLRELGSSEYHPYFTKRLVSMAMDRH 198

Qy  213 ASHREMTSKLLSDLCGTVMSTTDVEKSFDKLLKDLPELALDTPRAPQLVGQFIARAVGDG 272
Db  199 DKEKEMASVLLSALYADVILPDQIRDGFIRLRSVDDLAVDILDAVVNLALFIARAIVDE 258

Qy  273 ILCNTYI-----DSYKGTVDCVQARAALDKATVLLSMSKGGKRKDSVWGSGGGQQOSV 324
Db  259 ILPPVFLVRSKKILPESCKGFQVIVTAEKS------YLSAPHHAELVEKKWG--GSTHTTV 311

Qy  325 NHLVKEIDMLLKEYLLSGDISEAEHCLKELEVPHFHELVEYEAIIMVLES-TGESTFKMI 383
Db  312 EETKKKISEILKEYVENGDTYEACRCIRELGVSFFHHEVVKRALVLAMDSPTAES---LV 368

Qy  384 LDLLKSLWKSSTIIVDQMKRGYERIINEIPDINLDVPHSYSVLERFVEECFQAGIISKQL 443
Db  369 LKLKETAEEGLISSSQMVKGFFRVAESLDDLALDIPSAKKLFPDSIVPKAISGGWLDDSF 428

Qy  444 RDLCPSRGRKRFVSEGDG 461
Db  429 KITSDQDGEK---SSQDG 443
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RESULT 11
ID   Q9FMK4         PRELIMINARY;       PRT;    729 AA.
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RESULT 12
ID   080548         PRELIMINARY;       PRT;    693 AA.
AC   080548;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   T22J18.10 protein (Hypothetical 77.2 kDa protein).
GN   T22J18.10.
```

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OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Vysotskaia V.S., Schwartz J.R., Toriumi M., Yu G., Oji O., Kwan A.,
RA   Liu S., Li J., Araujo R., Au M., Brendel V., Conway A.B.,
RA   Conway A.R., Dewar K., Feng J., Kim C., Kurtz D., Li Y., Palm C.J.,
RA   Shinn P., Sun H., Davis R.W., Ecker J.R., Federspiel N.A.,
RA   Theologis A.;
RT   "Arabidopsis thaliana chromosome 1 BAC T22J18 sequence, complete
RT   sequence.";
RL   Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
RA   Goldsmith A.D., Lee J.M., Quach H.L., Tang C., Toriumi M., Yu G.,
RA   Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J.,
RA   Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Koesema E.,
RA   Lam B., Lin J., Meyers M.C., Miranda M., Natusaka M., Nguyen M.,
RA   Palm C.J., Sakurai T., Satou M., Seki M., Shinn P., Southwick A.,
RA   Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
RT   "Full Length cDNA of gene T22J18.10 (GI:3287683).";
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AC003979; AAC25511.1; -.
DR   EMBL; AY034972; AAK59477.1; -.
DR   InterPro; IPR003891; IF_eIF4G_MA3.
DR   Pfam; PF02847; MA3; 4.
DR   SMART; SM00544; MA3; 4.
KW   Hypothetical protein.
SQ   SEQUENCE 693 AA; 77244 MW; D5EE92BEEC190C15 CRC64;

Query Match     16.0%;  Score 386;  DB 10;  Length 693;
Best Local Similarity   28.2%;  Pred. No. 6.9e-19;
Matches 111;  Conservative 80;  Mismatches 168;  Indels 34;  Gaps 11;

Qy   77  VSDSGSDAL-RSGLTVPTS-----PKGRLLDRSRSGKGRGLPKKGGAGGKGVWGTPGQV 130
            ::!:! !:!  !:!      !|||!:!:! :!! !:! !|||!||:|:||
Db    6  LTIDSRKDPLCISQOLKISSSSLDPLPQANMAEDLTKSRRHSPIKVE---GSEETWGVE--- 59

Qy  131  YDVEEVDVKDPNYDDDQENCVYE-TVVLPLDERAFEKTLTPIIQEYFEHGDTNEVAEMLR 189
            :!! !| |!:   !  !:|| :|:|||||||||||||!|:!| !| !||!! :!
Db   60  ---DDDDLITDPIFDTIEGNGHSDPTSCFDADLSEYKKATVIVEEYFGTNDVSVVNELK 116

Qy  190  DLNLGEMKSGVPVLAVSLALEGKASHREMTSKLLSDLCGTVMSTTDVEKSFDKLLKDLPE 249
            !:! :||||||||||||||||:!: !  !!!| !!  !| !| :! |!|:!| |
Db  117  ELGMAEVRYEVKKLVSVNAMDRHDKEKEMAAFLLSTLYADVIDPPEVRGFNKLVASADD 176

Qy  250  LALDTPRAPQLVGQFIARAVGDGILCNTYI-------DSYKGTVDCVQARAALDKATVL 301
            !:!| !! ||!||||||||||!|:!|| :           !| |:!|| !| !:!::!
Db  177  LSVDIPDAVDLAVFVARAIVDDILPPAFLKKQMKLLPDNSKG----VEVLRKAEKS--Y 230

Qy  302  LSMSKGGRKDSVWGSGGGGQQOSVNHLVKEIDMLLKEYLLSGDISEAEHCLKELEVPHFHH 361
            !| !|!   ||  !   | !| !  !!|:|| !!|||!!| !!||||:| | |||:||
Db  231  LATPLHAEVVERWG-GYDNWTAEDVKARINDLLKEYVMSGDKKEAFRCIKGLKVPFFHH 289

Qy  362  ELVYEAIIMVLESTGESTFKMILDLLKSLWKSSTITVDQMKRGYERIYNEIPDINLDVPH 421
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  290  EIVKRALIMAMERRKAQV--RLLDLLKEFIEVGLINSTQVTKGFSRIIDSIEDLSLDIPD 347

Qy  422  SYSVLERFVEECFQAG-IISKQLRDICPSRGRK 453
            ||||||||||||||| !!!| ! !:! |:|| |
Db  348  ARRILQSFISKAASEGWLCASSLKSLSADAGEK 380
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RESULT 13
Q8W4Q4
ID   Q8W4Q4          PRELIMINARY;     PRT;   702 AA.
AC   Q8W4Q4;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
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DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   AT4g24800/F6I7_10.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
RA   Bowser L., Carninci P., Chen H., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
RA   Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
RA   Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
RA   Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
RA   Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
RA   Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
RA   Ecker J.R.;
RT   "Arabidopsis cDNA clones.";
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY062102; AAL32978.1; -.
DR   InterPro; IPR003891; IF_eIF4G_MA3.
DR   Pfam; PF02847; MA3; 4.
DR   SMART; SM00544; MA3; 4.
SQ   SEQUENCE 702 AA; 77435 MW; B7A3BC95488S4059 CRC64;

Query Match     15.3%;  Score 369;  DB 10;  Length 702;
Best Local Similarity   30.8%;  Pred. No. 1.1e-17;
Matches 108;  Conservative 59;  Mismatches 154;  Indels 30;  Gaps 10;

Qy  102  RSRSRSKGRGL-PKKGGAGGKGVWG-----TPGQVDYVEEVDVKDPNYDDDQE--NCYET 154
            |||| !||!| !||||||||||||      !||| !:!!| !|:|| !:!:    ! !
Db   54  KHRRSHAGRSIRSKKDGGGGKGNWGKLITDGDYH----IDPNDPNVDSGEEPFELVGAT 109

Qy  155  VVLPLDERAFEKTLTPIIQEYFEHGDTNEVAEMLRDLNLGEMKSGVPVLAVSLALEGKAS 214
            !||| :! |:| !!|!|||!||:!|| !|:| !:!| !  !|| |||||||:| !!::
Db  110  LSDPLDD--YKKAAASIINEYFSTGDVDVAAADLIELGSSEYHPYFIKRLVSVAMDRHDK 167

Qy  215  HREMTSKLLSDLCGTVMSTTDVEKSFDKLLKDLPELALDTPRAPQLVGQFIARAVGDGIL 274
            |:||  !|| !  !| !!|| ! |!|  !|!| |  !|| !  ! ! | !||||| |:||
Db  168  EKEMASVLLSALYADVINPNQIRDGFVLLESADFVVDIPDAVNVLALFLARAVVDDIL 227

Qy  275  CNTYID--------SYKGTVDCVQARAALDKATVLLSMSKGGRKDSVWGSGGGGQQOSVNH 326
            ! :  |        !:! !  |! |!   ! !|  |! |!   ||   | !   | !:!!
Db  228  PPAFLPRAAKALPITSKG----YQVVQTAEKS--YLSAAHHARLVERRWG-GQTRTIVEE 280

Qy  327  LVKEIDMLLKEYLLSGDISEAEHCLKELEVPHFHHELVYEAIIMVLESTGESTFKMILDL 386
            ! |!| !| ||! :| ! |||:| | |||:||:||| :!:! !!|| |: !  !!!|
Db  281  VKKKIADILNEYVETGETYEACRCVRELGVSFFHHEVVKRALVTALEN--HAAEAPVLKL 338

Qy  387  LKSLWKSSTITVDQMKRGYERIYNEIPDINLDVPHSYSVLERFVEECFQAG 437
            ! !! !| :  | !| |!| |:!| !| ! | !   ! |!|! ! !  !||
Db  339  LNEAASENLISSSQMVGFSRLRESDLDDLALDIPSARFKGLIVPKAVSGG 389
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RESULT 14
Q9SZX0
ID   Q9SZX0          PRELIMINARY;     PRT;   942 AA.
AC   Q9SZX0;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Hypothetical 104.9 kDa protein.
GN   F6I7.10 OR AT4G24800.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Bevan M., Terryn N., Ardiles W., Buysshaert C., Dasseville R.,
RA   De Clerck R., De Keyser A., Neyt P., Rouze P., Van Den Daele H.,
RA   Villaroel R., Gielen J., Van Montagu M., Bancroft I., Hoheisel J.,
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RA   Mewes H.W., Mayer K.F.X., Schueller C.;
RL   Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   EU Arabidopsis sequencing project;
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RA   EU Arabidopsis sequencing project;
RL   Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
RP   SEQUENCE FROM N.A.
DR   EMBL; AL049657; CAB41120.1; -.
DR   EMBL; AL161562; CAB79390.1; -.
DR   InterPro; IPR003891; IF_eIF4G_MA3.
DR   Pfam; PF02847; MA3; 4.
DR   SMART; SM00544; MA3; 4.
KW   Hypothetical protein.
SQ   SEQUENCE   942 AA; 104913 MW; 93575FEBBA1EFCE0 CRC64;

Query Match   15.3%;   Score 369; DB 10; Length 942;
Best Local Similarity   30.8%; Pred. No. 1.8e-17;
Matches 108; Conservative 59; Mismatches 154; Indels 30; Gaps 10;

Qy 102 RRSRSGKGRGL-PKKGGAGGKGVWG-----TPGQVYDVEEVDVKDPNYDDDQE--NCVYET 154
         || : | ||| : || :|| | : | | | || ||
Db   54 KHRRSHAGRSIRSKKDGGGKGNWGKLIDTDGYH----IDPNDPNVDSGEBPFELVGAT 109

Qy 155 VVLPLDERAFEKTLTPIIQEYFEHGDTNEVAEMLRDLNIGEMKSGVPVLAVSLALEGKAS 214
Db 110 LSDPLDD--YKKAAASIINEYFSTGDVDVAAADLIELGSSSEYHPYFIKRLVSVAMDRHDK 167

Qy 215 HREMTSKLLSDLCGTVMSTTDVEKSFDKLLKDLPELALDTPRAPOLVGQFIARAVGDGIL 274
Db 168 EKEMASVLLSALYADVINPNQIRDGFVLLESADDFVVDIPDAVNVLALFLARAVVDDIL 227

Qy 275 CNTYID--------SYKGTVDCVQARAALDKATVLLSMSKGGKRKDSVWGSGGGQQOSVNH 326
Db 228 PPAFLPRAAKALPITSKG----YQVVQTAEKS--YLSAAHHAELVERRWG-GQTRTTVEE 280

Qy 327 LVKEIDMLLKEYLLSGDISEAEHCLKELEVPHFHHELVYEAIIMVLSTGESTFKMIDLL 386
Db 281 VKKIADILNEEVEYGETYEACRCVRELGVSFFHHEVVKRALVTALEN--HAABAPVLKL 338

Qy 387 LKSLWKSSTITVDQMKRGYERIYNEIPDINLDVPHSYSVLERFVEECFQAG 437
Db 339 LNEAASENLISSSQMVKGFSRLRESLDDLALDIPSARFKFGLIVPKAVSGG 389

RESULT 15
O64378
ID   O64378
AC   O64378;
DT   01-AUG-1998 (TrEMBLrel. 07, Created)
DT   01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Putative topoisomerase (Fragment).
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. COLUMBIA;
RX   MEDLINE=98034136; PubMed=9369203;
RA   Terryn N., Neyt P., De Clercq R., De Keyser A., Van Den Daele H.,
RA   Ardiles W., Dehais P., Rouze P., Gielen J., Villarroel R.,
RA   Van Montagu M.;
RT   "Sequence analysis of a 24kb contig downstream of Pfl1, located on
RT   chromosome I."
RL   FEBS Lett. 416:156-160(1997).
DR   EMBL; Y12227; CAA72903.1; -.
DR   InterPro; IPR003891; IF_eIF4G_MA3.
DR   Pfam; PF02847; MA3; 4.
DR   SMART; SM00544; MA3; 4.
KW   Isomerase.
FT   NON_TER   1
SQ   SEQUENCE   618 AA; 69282 MW; BDAACAE801C26679 CRC64;

Query Match   15.1%;   Score 364; DB 10; Length 618;
Best Local Similarity   30.7%; Pred. No. 2.1e-17;
Matches 93; Conservative 61; Mismatches 131; Indels 18; Gaps 6;

Qy 160 DERAFEKTLTPIIQEYFEHGDTNEVAEMLRDLNIGEMKSGVPVLAVSLALEGKASHREMT 219
Db   9 DLSEYKKKATVIVEEYFGTNDVVSVVNELKELGMAEYRYIFVKKLVSMAMDRHDKEKEMA 68

Qy 220 SKLLSDLCGTVMSTTDVEKSFDKLLKDLPELALDTPRAPOLVGQFIARAVGDGILCNTYI 279
Db   69 AFLLSTLYADVIDPPEVYRGFNKLVASADDLSVDIPDAVDVLAVEVARAIVDDILPPAFL 128

Qy 280 -------DSYKGTVDCVQARAALDKATVLLSMSKGGKRKDSVWGSGGGGQQOSVNHLVKEI 331
Db 129 KKQMKLLPDNSKG----VEVLRKAEKS--YLATPLHAEVVEKRWG-GTDNWTAEDVKARI 181

Qy 332 DMLLKEYLLSGDISEAEHCLKELEVPHFHHELVYEAIIMVLESTGESTFKMIDLLKSLW 391
Db 182 NDLLKEYVMSGDKKEAFRCIKGLKVPFFHHEIVKRALIMAMERRAQV--RLLDLLKETI 239

Qy 392 KSSTITVDQMKRGYERIYNEIPDINLDVPHSYSVLERFVEECFQAG-IISKQLRDLCPSR 450
Db 240 EVGLINSTQVTKGFSRIIDSTEDLSLDIPDARRILQSFISKAASEGWLCASSLKSLSADA 299

Qy 451 GRK 453
Db 300 GEK 302

Search completed: January 24, 2003, 17:29:42
Job time : 40 secs